HIDI: Genomics, Metagenomics & Data Analysis

Deep Immune Phenotyping

Genomics, Metagenomics & Data Analysis

Immune Imaging

Proteomics

Dr Camilla Ip

Dr Calliope Dendrou

HIDI Day

1 October 2018

Medical Sciences Training Centre

University of Oxford

HIDI Aims

Facilitate access
to immunological expertise
in the form of:

1. funding,
2. experimental equipment and expert advice, and
3. **data management, analysis and cross-platform analyses**

to improve

- immunological capability in Oxford,
- communication & collaboration in Oxford,
- new discoveries, &
- patient outcomes.

The HIDI Platforms

Deep Immune Phenotyping

Immune cell phenotyping, cytokine staining, immunoassays

Genomics, Metagenomics & Data Analysis

Immunogenomics (DNA/RNA/TCR-BCR/protein analysis), Viromics/Microbiomics pipeline (sequencing + analysis), Metabolomics (mass spectrometry)

Immune Imaging

Chip cytometry, multi-spectral imaging, electron microscopy, micron advanced bioimaging unit, live-cell super-resolution microscopy

Proteomics

Immunopeptidomics

Genomics, Metagenomics & Data Analysis

Calli Dendrou

Group Leader, WHG

- Immune-mediated diseases
- Primary human immune cell genotype-to-phenotype analyses
- Disease gene regulation
- Immune gene expression dynamics

Camilla Ip

Bioinformatician, Dendrou Group

- Bioinformatics pipelines
- Microbial genomics
  - ModMedMicro Consortium
  - WHG Bioinformatics Core
  - STOP-HCV Consortium
- Data management
- Databases
- Nanopore data analysis

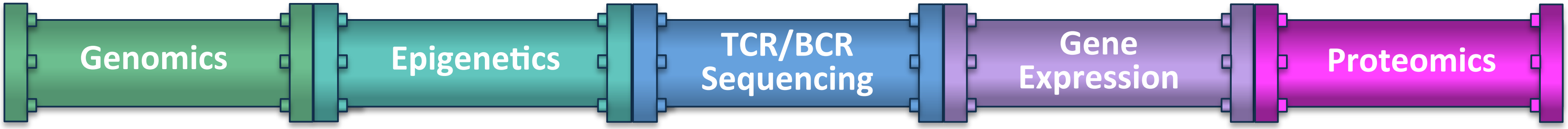
Experimental design

Data analysis comes last but do contact us from the start - before you begin experiments

No question is too trivial

- How to choose the right technology?
- How many samples/cells for appropriate power?
- How many replicates?
- How to design experiments to minimise artefacts in resulting data?
- How to mine and make use of available data sets?
- How to maximise output given funds available?

Techniques supported



Genomics

Epigenetics

TCR/BCR Sequencing

Gene Expression

Proteomics

- Whole exome sequencing
- Whole genome sequencing
- Targeted gene sequencing
- Genotyping
- DNA/RNA metagenomics – species identification

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Epigenetics

- Regulatory element identification (e.g. DNase HS, ATAC-Seq)
- ChIP-Seq
- Bisulfite-Seq
- Chromatin conformation capture
- Data mining

ROADMAP epigenomics PROJECT

BLUEPRINT epigenome

TCR/BCR Sequencing

Gene Expression

Proteomics

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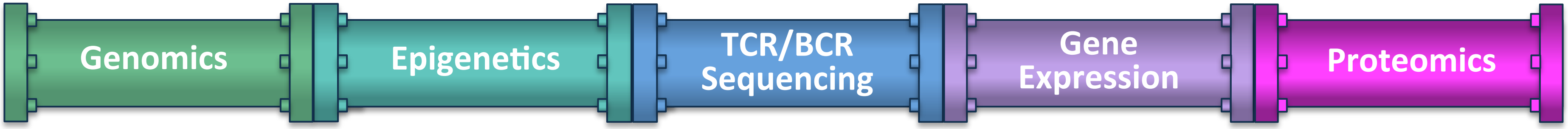

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- Single-cell V(D)J-Seq +/- 5’ mRNA-Seq

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- Bulk RNA-Seq
- 3’/5’ scRNA-Seq
- CITE-Seq
- Demultiplexing & deconvolution

10x GENOMICS

BD Rhapsody

illumina

Proteomics

Techniques supported

wellcome centre human genetics

UNIVERSITY OF OXFORD

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BLUEPRINT EU epigenome

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10X GENOMICS

BD Rhapsody

illumina

Proteomics

- Proteome lists to guide MS interpretation
- Proteome characterisation from MS

Additional expertise

Next Gen Sequencing

- Oxford Genomics Centre (David Buck, Helen Lockstone, Rory Bowden, WHG)

Single-Cell Genomics

- Oxford Single Cell Consortium (Neil Ashley, WIMM; Rory Bowden, WHG)

Oxford Viromics Pipeline

- David Bonsall (BDI); Rory Bowden (WHG)

Microbiomics

- Claire Pearson (Kennedy)

Metabolomics

- James McCullagh (Chemistry)

Proteomics

- Nicola Ternette (Jenner/TDI)

Data analysis across multiple platforms

Data management

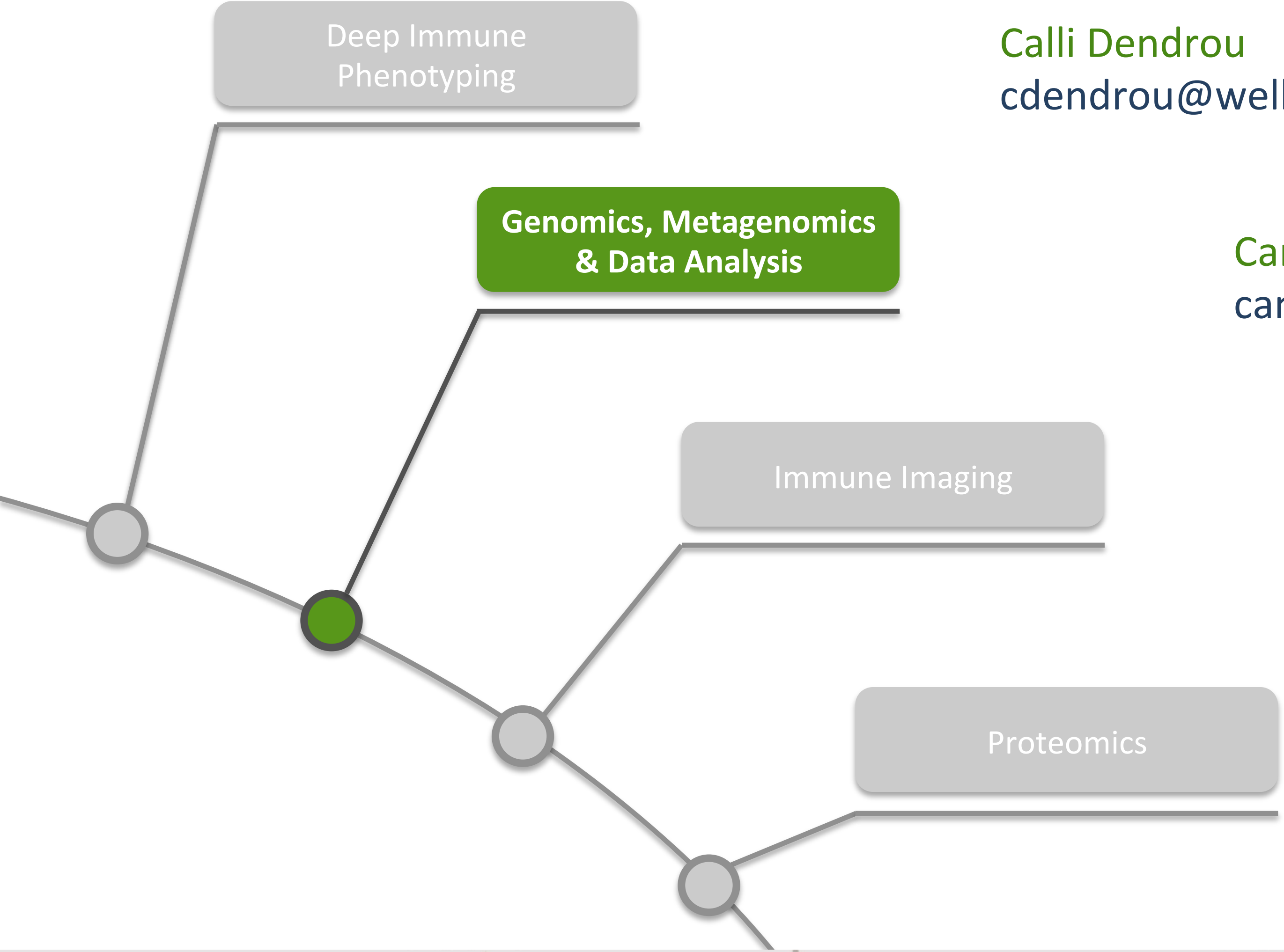
- Initial storage and pre-processing of raw data
- Integration of data from multiple platforms

Cross-platform analyses

Collaboration and documentation tools

- HIDIbook : *LabArchives* notebook for project documentation and collaboration
- HIDIproject : *Slack* workspace for team messaging and teleconferencing
- HIDIcode : *GitHub* repository for code distribution

Contact us



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